THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A conformationally constrained compound or a pharmaceutically acceptable salt or prodrug thereof, the compound comprising an amino acid sequence (I):

(I) R-(Haa_1-Saa-Xaa_1-Xaa_2)$_n$-Haa_2-Xaa_3-Xaa_4-Haa_3-(Saa-Naa-Xaa_5-Haa_4)$_m$-R'

wherein Haa_1, Haa_2, Haa_3 and Haa_4 are each independently an amino acid residue with a hydrophobic side chain or when n and m are both 1, one of Haa_1, Haa_2 and Haa_4 is optionally Xaa_1;

each Saa is an amino acid residue with a small side chain;

Naa is an amino acid residue with a negatively charged side chain;

Xaa_1, Xaa_2, Xaa_3, Xaa_4 and Xaa_5 are each independently an amino acid residue, Zaa_1 or Zaa_2;

R is H, an N-terminal capping group or an oligopeptide optionally capped by an N-terminal capping group;

R' is H, a C-terminal capping group or an oligopeptide optionally capped by a C-terminal capping group; and

m and n are 0 or 1, provided that at least one of m and n is 1;

wherein a conformational constraint is provided by a linker (L) which tethers two amino acid residues, Zaa_1 and Zaa_2, in the sequence.

2. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein all of Haa_1, Haa_2, Haa_3 and Haa_4 are amino acid residues with a hydrophobic side chain.

3. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein Haa_1, Haa_2, Haa_3 and Haa_4 are independently selected from L-phenylalanine, L-isoleucine, L-leucine, L-valine, L-methionine and L-tyrosine.

4. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein Haa_2 is L-leucine.

5. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein each Saa is independently selected from glycine, L-alanine, L-serine, L-cysteine and aminoisobutyric acid.

6. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein Naa is an L-aspartic acid or an L-glutamic acid residue.

7. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein R is an N-terminal capping group or an oligopeptide having 1 to 10 amino acid residues selected from Xaa_1, optionally capped with an N-terminal capping group.

8. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 7 wherein R is an N-terminal capping group selected from acyl and N-succinate.

9. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein R' is a C-terminal capping group or an oligopeptide having 1 to 10 amino acid residues selected from Xaa_1, optionally capped with a C-terminal capping group.

10. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 9, wherein the C-terminal capping group is NH_2.

11. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1, wherein Xaa_1, Xaa_2, Xaa_3, Xaa_4 and Xaa_5 are independently selected from L-alanine, L-arginine, L-asparagine, L-aspartic acid, L-

cysteine, L-glutamine, L-glutamic acid, L-glycine, L-histidine, L-isoleucine, L-leucine, L-lysine, L-methionine, L-phenylalanine, L-proline, L-serine, L-threonine, L-tryptophan, L-tyrosine and L-valine.

12. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein the linker (L) tethers two non-adjacent amino acids in an i(i+7) relationship where the first end of the linker is attached to a first amino acid residue (Zaa_1) at a first position and the other end of the linker is attached to a second amino acid residue (Zaa_2) which is positioned 7 amino acids after Zaa_1.

13. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein L is 4 to 8 atoms in length.

14. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 12 wherein Zaa_1 is located before Haa_1 at the N-terminal of the sequence and Zaa_2 is located between Haa_2 and Haa_3.

15. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 12 wherein Zaa_1 is located between Haa_1 and Haa_2 and Zaa_2 is located between Haa_3 and Haa_4.

16. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 12 wherein Zaa_1 is located between Haa_2 and Haa_3 and Zaa_2 is located after Haa_4 at the C-terminal end of the amino acid sequence.

17. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein Zaa_1 and Zaa_2 are independently selected from L-aspartic acid, L-glutamic acid, L-lysine, L-ornithine, D-aspartic acid, D-glutamic acid, D-lysine, D-ornithine, L-β-homoaspartic acid, L-β-homoglutamic acid, L-β-homolysine, L-α-methylaspartic acid, L-α-methylglutamic acid, L-α-methyllysine, L-α-methylornithine, D-α-methylaspartic acid, D-α-methylglutamic acid, D-α-methyllysine

and L-α-methylornithine.

18. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 17 wherein Zaa_1 and Zaa_2 are independently selected from L-aspartic acid, L-glutamic acid, L-lysine and L-ornithine.

19. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 18 wherein Zaa_1 and Zaa_2 are independently selected from L-aspartic acid and L-glutamic acid.

20. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein Zaa_1 and Zaa_2 have side chains containing a carboxylic acid and the linker is selected from the group consisting of $-NH(CH_2)_4NH-$, $-NH(CH_2)_5NH-$, $-NH(CH_2)_6NH-$, $-NH(CH_2)_7NH-$, $-NH(CH_2)_2O(CH_2)_2NH-$, $-NH(CH_2)_2N^+H_2(CH_2)_2NH-$, $-NH(CH_2)_2S(CH_2)_2NH-$, $-NHCH_2C(=O)NH(CH_2)_2NH-$, $-NH(CH_2)_2NHC(=O)CH_2NH-$, $-NH(CH_2)_2SS(CH_2)_2-NH-$, $-NH(CH_2)_2O(CH_2)_3NH-$, $-NH(CH_2)_2N^+H_2(CH_2)_3NH-$, $-NH(CH_2)_2S(CH_2)_3NH-$, $-NH(CH_2)_2C(=O)NH(CH_2)_2NH-$, $-NH(CH_2)_2NHC(=O)(CH_2)_2NH-$, $-NHCH_2C(=O)NH(CH_2)_3NH-$, $-NH(CH_2)_3NHC(=O)CH_2NH-$, $-NHCH_2C(=O)NH(CH_2)_4NH-$, $-NH(CH_2)_4NHC(=O)CH_2NH-$, $-NH(CH_2)_2C(=O)NH(CH_2)_3NH-$, $-NH(CH2)_3NHC(=O)(CH_2)_2NH-$, $-NH(CH_2)_3C(=O)NH(CH_2)_2NH-$ and $-NH(CH_2)_2NHC(=O)(CH_2)_3NH-$.

21. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 20 wherein the linker is selected from the group consisting of $-NH(CH_2)_5NH-$, $-NH(CH_2)_6NH-$, $-NH(CH_2)_7NH-$, $-NHCH_2C(=O)NH(CH_2)_2NH-$, $-NH(CH_2)_2NHC(=O)CH_2NH-$, $-NH(CH_2)_2O(CH_2)_3NH-$ and $-NH(CH_2)_2C(=O)NH(CH_2)_2NH-$.

22. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 20 wherein the linker is selected from the group

consisting of –$NH(CH_2)_5NH$- and –$NHCH_2C(=O)NH(CH_2)_2NH$-.

23. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein Zaa_1 and Zaa_2 have side chains containing an amino group and the linker is selected from the group consisting of -$C(=O)(CH_2)_4C(=O)$-, -$C(=O)(CH_2)_5C(=O)$-, -$C(=O)(CH_2)_6C(=O)$-, -$C(=O)(CH_2)_7C(=O)$-, -$C(=O)(CH_2)_2O(CH_2)_2C(=O)$-, -$C(=O)(CH_2)N^+H_2(CH_2)_2C(=O)$-, -$C(=O)(CH_2)S(CH_2)_2C(=O)$-, -$C(=O)CH_2C(=O)NH(CH_2)_2C(=O)$-, -$C(=O)(CH_2)_2NHC(=O)CH_2C(=O)$-, -$C(=O)(CH_2)_2SS(CH_2)_2$-$C(=O)$-, -$C(=O)(CH_2)_2O(CH_2)_3C(=O)$-, -$C(=O)(CH_2)_2N^+H_2(CH_2)_3C(=O)$-, -$C(=O)(CH_2)_2S(CH_2)_3C(=O)$-, -$C(=O)(CH_2)_2C(=O)NH(CH_2)_2C(=O)$-, -$C(=O)(CH_2)_2NHC(=O)(CH_2)_2C(=O)$-, -$C(=O)CH_2C(=O)NH(CH_2)_3C(=O)$-, -$C(=O)(CH_2)_3NHC(=O)CH_2C(=O)$-, -$C(=O)CH_2C(=O)NH(CH_2)_4C(=O)$-, -$C(=O)(CH_2)_4NHC(=O)CH_2C(=O)$-, -$C(=O)(CH_2)_2C(=O)NH(CH_2)_3C(=O)$-, -$C(=O)(CH2)_3NHC(=O)(CH_2)_2C(=O)$-, -$C(=O)(CH_2)_3C(=O)NH(CH_2)_2C(=O)$- and -$C(=O)(CH_2)_2NHC(=O)(CH_2)_3C(=O)$-.

24. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 23 wherein the linker is selected from the group consisting of –$C(=O)(CH_2)_5C(=O)$-, -$C(=O)(CH_2)_6C(=O)$-, -$C(=O)(CH_2)_7C(=O)$-, -$C(=O)CH_2C(=O)NH(CH_2)_2C(=O)$-, -$C(=O)(CH_2)_2NHC(=O)CH_2C(=O)$-, -$C(=O)(CH_2)_2O(CH_2)_3C(=O)$- and –$C(=O)(CH_2)_2C(=O)NH(CH_2)_2C(=O)$-.

25. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 23 wherein the linker is selected from the group consisting of -$C(=O)(CH_2)_5C(=O)$- and -$C(=O)CH_2C(=O)NH(CH_2)_2C(=O)$-.

26. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein Zaa_1 has a side chain containing an amino group and Zaa_2 has a side chain containing a carboxylic acid and the linker is selected -$C(=O)(CH_2)_4NH$-, -$C(=O)(CH_2)_5NH$-, -$C(=O)(CH_2)_6NH$-, -$C(=O)(CH_2)_7NH$-,

$-C(=O)(CH_2)_2O(CH_2)_2NH-$, $-C(=O)(CH_2)N^+H_2(CH_2)_2NH-$, $-C(=O)(CH_2)S(CH_2)_2NH-$, $-C(=O)CH_2C(=O)NH(CH_2)_2NH-$, $-C(=O)(CH_2)_2NHC(=O)CH_2NH-$, $-C(=O)(CH_2)_2SS(CH_2)_2-NH-$, $-C(=O)(CH_2)_2O(CH_2)_3NH-$, $-C(=O)(CH_2)_2N^+H_2(CH_2)_3NH-$, $-C(=O)(CH_2)_2S(CH_2)_3NH-$, $-C(=O)(CH_2)_2C(=O)NH(CH_2)_2NH-$, $-C(=O)(CH_2)_2NHC(=O)(CH_2)_2NH-$, $-C(=O)CH_2C(=O)NH(CH_2)_3NH-$, $-C(=O)(CH_2)_3NHC(=O)CH_2NH-$, $-C(=O)CH_2C(=O)NH(CH_2)_4NH-$, $-C(=O)(CH_2)_4NHC(=O)CH_2NH-$, $-C(=O)(CH_2)_2C(=O)NH(CH_2)_3NH-$, $-C(=O)(CH2)_3NHC(=O)(CH_2)_2NH-$, $-C(=O)(CH_2)_3C(=O)NH(CH_2)_2NH-$ and $-C(=O)(CH_2)_2NHC(=O)(CH_2)_3NH-$.

27. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 26 wherein the linker is selected from the group consisting of $-C(=O)(CH_2)_5NH-$, $-C(=O)(CH_2)_6NH-$, $-C(=O)(CH_2)_7NH-$, $-C(=O)CH_2C(=O)NH(CH_2)_2NH-$, $-C(=O)(CH_2)_2NHC(=O)CH_2NH-$, $-C(=O)(CH_2)_2O(CH_2)_3NH-$ and $-C(=O)(CH_2)_2C(=O)NH(CH_2)_2NH-$.

28. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 26 wherein the linker is selected from the group consisting of $-C(=O)(CH_2)_5NH-$ and $-C(=O)CH_2C(=O)NH(CH_2)_2NH-$.

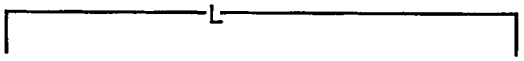
29. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 wherein Zaa_1 has a side chain containing a carboxylic acid and Zaa_2 has a side chain containing an amino group and the linker is selected from the group consisting of $-NH(CH_2)_4C(=O)-$, $-NH(CH_2)_5C(=O)-$, $-NH(CH_2)_6C(=O)-$, $-NH(CH_2)_7C(=O)-$, $-NH(CH_2)_2O(CH_2)_2C(=O)-$, $-NH(CH_2)N^+H_2(CH_2)_2C(=O)-$, $-NH(CH_2)S(CH_2)_2C(=O)-$, $-NHCH_2C(=O)NH(CH_2)_2C(=O)-$, $-NH(CH_2)_2NHC(=O)CH_2C(=O)-$, $-NH(CH_2)_2SS(CH_2)_2C(=O)-$, $-NH(CH_2)_2O(CH_2)_3C(=O)-$, $-NH(CH_2)_2N^+H_2(CH_2)_3C(=O)-$, $-NH(CH_2)_2S(CH_2)_3C(=O)-$, $-NH(CH_2)_2C(=O)NH(CH_2)_2C(=O)-$, $-NH(CH_2)_2NHC(=O)(CH_2)_2C(=O)-$, $-NHCH_2C(=O)NH(CH_2)_3C(=O)-$, $-NH(CH_2)_3NHC(=O)CH_2C(=O)-$, $-NHCH_2C(=O)NH(CH_2)_4C(=O)-$, $-NH(CH_2)_4NHC(=O)CH_2C(=O)-$,

$-NH(CH_2)_2C(=O)NH(CH_2)_3C(=O)-$, $-NH(CH_2)_3NHC(=O)(CH_2)_2C(=O)-$, $-NH(CH_2)_3C(=O)NH(CH_2)_2C(=O)-$.

30. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 29 wherein the linker is selected from the group consisting of $-NH(CH_2)_5C(=O)-$, $-NH(CH_2)_6C(=O)-$, $-NH(CH_2)_7C(=O)-$, $-NHCH_2C(=O)NH(CH_2)_2C(=O)-$, $-NH(CH_2)_2NHC(=O)CH_2C(=O)-$, $-NH(CH_2)_2O(CH_2)_3C(=O)-$ and $-NH(CH_2)_2C(=O)NH(CH_2)_2C(=O)-$.

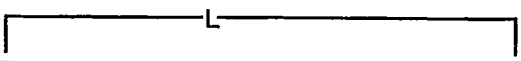
31. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 29 wherein the linker is selected from the group consisting of $-NH(CH_2)_5C(=O)-$ and $-NHCH_2C(=O)NH(CH_2)_2C(=O)-$.

32. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1, of any one of formulae (II) to (VI):



(II) R^1-Zaa_1-Haa_1-Saa-Xaa_1-Xaa_2-Haa_2-Xaa_3-Zaa_2-Haa_3-(Saa-Naa-Xaa_5-Haa_4)$_m$-$R^{1'}$

wherein Haa_1, Haa_2, Haa_3, Haa_4, Xaa_1, Xaa_2, Xaa_3, Xaa_5, Saa, Naa and L are as defined above for formula (I), m is 0 or 1, R^1 and $R^{1'}$ are as defined above for R and R' in formula (I), Zaa_1-L-Zaa_2 represents two amino acid residues with their side chains bridged by a linker L;



(III) R^2-Zaa_1-Xaa_6-Haa_1-Saa-Xaa_1-Xaa_2-Haa_2-Zaa_2-Xaa_4-Haa_3-(Saa-Naa-Xaa_5-Haa_4)$_m$-$R^{2'}$

wherein Haa_1, Haa_2, Haa_3, Haa_4, Xaa_1, Xaa_2, Xaa_4, Xaa_5, Saa, Naa and L are as defined above for formula (I), Xaa_6 is an amino acid residue as defined for Xaa_1 above; m is 0 or 1, R^2 and $R^{2'}$ are as defined above for R and R' in formula (I), Zaa_1-L-Zaa_2 represents two amino acid residues with their side chains bridged by a linker L;

(IV) R^3-(Haa_1-Saa-Xaa_1)$_p$-Zaa_1-Haa_2-Xaa_3-Xaa_4-Haa_3-Saa-Naa-Zaa_2-Haa_4-$R^{3'}$ (L bridging Zaa_1 and Zaa_2)

wherein Haa_1, Haa_2, Haa_3, Haa_4, Xaa_1, Xaa_3, Xaa_4, Saa, Naa and L are as defined above for formula (I), p is 0 or 1, R^3 and $R^{3'}$ are as defined above for R and R' in formula (I), Zaa_1-L-Zaa_2 represents two amino acid residues with their side chains bridged by a linker L;

(V) R^4-(Haa_1-Saa-Xaa_1-Xaa_2)$_n$-Haa_2-Zaa_1-Xaa_4-Haa_3-Saa-Naa-Xaa_5-Haa_4-Zaa_2-$R^{4'}$ (L bridging Zaa_1 and Zaa_2)

wherein Haa_1, Haa_2, Haa_3, Haa_4, Xaa_1, Xaa_2, Xaa_4, Xaa_5, Saa, Naa and L are as defined above in formula (I), n is 0 or 1, R^4 and $R^{4'}$ are as defined above for R and R' in formula (I), Zaa_1-L-Zaa_2 represents two amino acid residues with their side chains bridged by a linker L; and

(VI) R^5-(Haa_1-Saa-Xaa_1-Xaa_2)$_n$-Haa_2-Xaa_3-Zaa_1-Haa_3-Saa-Naa-Xaa_5-Haa_4-Xaa_6-Zaa_2-$R^{5'}$ (L bridging Zaa_1 and Zaa_2)

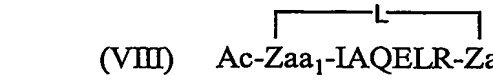
wherein Haa_1, Haa_2, Haa_3, Haa_4, Xaa_1, Xaa_2, Xaa_3, Xaa_5, Saa, Naa and L are as defined above for formula (I), Xaa_6 is an amino acid residue as defined for Xaa_1 above; n is 0 or 1, R^5 and $R^{5'}$ are as defined above for R and R' in formula (I), Zaa_1-L-Zaa_2 represents two amino acid residues with their side chains bridged by a linker L; or a pharmaceutically acceptable salt or prodrug thereof.

33. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 32 having structural formula (VII):

(VII) R^3-Zaa_1-Haa_2-Xaa_3-Xaa_4-Haa_3-Saa-Naa-Zaa_2-Haa_4-$R^{3'}$ (L bridging Zaa_1 and Zaa_2)

wherein Zaa_1, Haa_2, Xaa_3, Xaa_4, Haa_3, Saa, Naa, Zaa_2, Haa_4, R^3, $R^{3'}$ and L are defined above in formula (IV).

34. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 having structural formula (VIII):



(VIII) Ac-Zaa_1-IAQELR-Zaa_2-IGDEF-NH_2

where Zaa_1 and Zaa_2 are selected from L-aspartic acid, L-glutamic acid; and

L is selected from $-NH(CH_2)_4NH-$, $-NH(CH_2)_5NH-$, $-NH(CH_2)_6NH-$, $-NH(CH_2)_7NH-$, $-NH(CH_2)_2O(CH_2)_2NH-$, $-NH(CH_2)N^+H_2(CH_2)_2NH-$, $-NH(CH_2)S(CH_2)_2NH-$, $-NHCH_2C(=O)NH(CH_2)_2NH-$, $-NH(CH_2)_2NHC(=O)CH_2NH-$, $-NH(CH_2)_2SS(CH_2)_2NH-$, $-NH(CH_2)_2O(CH_2)_3NH-$, $-NH(CH_2)_2N^+H_2(CH_2)_3NH-$, $-NH(CH_2)_2S(CH_2)_3NH-$, $-NH(CH_2)_2C(=O)NH(CH_2)_2NH-$ and $-NH(CH_2)_2NHC(=O)(CH_2)_2NH-$; or

where Zaa_1 and Zaa_2 are selected from L-lysine and ornithine; and

L is selected from $-C(=O)(CH_2)_4C(=O)-$, $-C(=O)(CH_2)_5C(=O)-$, $-C(=O)(CH_2)_6C(=O)-$, $-C(=O)(CH_2)_7C(=O)-$, $-C(=O)(CH_2)_2O(CH_2)_2C(=O)-$, $-C(=O)(CH_2)N^+H_2(CH_2)_2C(=O)-$, $-C(=O)(CH_2)S(CH_2)_2C(=O)-$, $-C(=O)CH_2C(=O)NH(CH_2)_2C(=O)-$, $-C(=O)(CH_2)_2NHC(=O)CH_2C(=O)-$, $-C(=O)(CH_2)_2SS(CH_2)_2C(=O)-$, $-C(=O)(CH_2)_2O(CH_2)_3C(=O)-$, $-C(=O)(CH_2)_2N^+H_2(CH_2)_3C(=O)-$, $-C(=O)(CH_2)_2S(CH_2)_3C(=O)-$, $-C(=O)(CH_2)_2C(=O)NH(CH_2)_2C(=O)-$ and $-C(=O)(CH_2)_2NHC(=O)(CH_2)_2C(=O)-$; or

where Zaa_1 is selected from L-aspartic acid, L-glutamic acid and Zaa_2 is selected from L-lysine and ornithine; and

L is selected from $-NH(CH_2)_4C(=O)-$, $-NH(CH_2)_5C(=O)-$, $-NH(CH_2)_6C(=O)-$, $-NH(CH_2)_7C(=O)-$, $-NH(CH_2)_2O(CH_2)_2C(=O)-$, $-NH(CH_2)N^+H_2(CH_2)_2C(=O)-$, $-NH(CH_2)S(CH_2)_2C(=O)-$, $-NHCH_2C(=O)NH(CH_2)_2C(=O)-$, $-NH(CH_2)_2NHC(=O)CH_2C(=O)-$, $-NH(CH_2)_2SS(CH_2)_2C(=O)-$, $-NH(CH_2)_2O(CH_2)_3C(=O)-$, $-NH(CH_2)_2N^+H_2(CH_2)_3C(=O)-$, $-NH(CH_2)_2S(CH_2)_3C(=O)-$, $-NH(CH_2)_2C(=O)NH(CH_2)_2C(=O)-$ and $-NH(CH_2)_2NHC(=O)(CH_2)_2C(=O)-$; or

where Zaa_1 is selected from L-lysine and ornithine and Zaa_2 is selected from L-aspartic acid, L-glutamic acid; and

L is selected from $-C(=O)(CH_2)_4NH-$, $-C(=O)(CH_2)_5NH-$, $-C(=O)(CH_2)_6NH-$,

-C(=O)$(CH_2)_7$NH-, -C(=O)$(CH_2)_2O(CH_2)_2$NH-, -C(=O)$(CH_2)N^+H_2(CH_2)_2$NH-, -C(=O)$(CH_2)S(CH_2)_2$NH-, -C(=O)$CH_2C(=O)NH(CH_2)_2$NH-, -C(=O)$(CH_2)_2NHC(=O)CH_2$NH-, -C(=O)$(CH_2)_2SS(CH_2)_2$NH-, -C(=O)$(CH_2)_2O(CH_2)_3$NH-, -C(=O)$(CH_2)_2N^+H_2(CH_2)_3$NH-, -C(=O)$(CH_2)_2S(CH_2)_3$NH-, -C(=O)$(CH_2)_2C(=O)NH(CH_2)_2$NH- and –C(=O)$(CH_2)_2NHC(=O)(CH_2)_2$NH-.

35. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 having structural formula (IX):

(IX) Ac-IAQ-Zaa-LRRIGD-Zaa-F-NH_2 (L bridging the two Zaa)

where Zaa_1 and Zaa_2 are selected from L-aspartic acid, L-glutamic acid; and

L is selected from –$NH(CH_2)_4$NH-, -$NH(CH_2)_5$NH-, -$NH(CH_2)_6$NH-, -$NH(CH_2)_7$NH-, -$NH(CH_2)_2O(CH_2)_2$NH-, -$NH(CH_2)N^+H_2(CH_2)_2$NH-, -$NH(CH_2)S(CH_2)_2$NH-, -$NHCH_2C(=O)NH(CH_2)_2$NH-, -$NH(CH_2)_2NHC(=O)CH_2$NH-, -$NH(CH_2)_2SS(CH_2)_2$NH-, -$NH(CH_2)_2O(CH_2)_3$NH-, -$NH(CH_2)_2N^+H_2(CH_2)_3$NH-, -$NH(CH_2)_2S(CH_2)_3$NH-, -$NH(CH_2)_2C(=O)NH(CH_2)_2$NH-, -$NH(CH_2)_2NHC(=O)(CH_2)_2$NH-, -$NHCH_2C(=O)NH(CH_2)_3$NH-, -$NH(CH_2)_3NHC(=O)CH_2$NH-, -$NHCH_2C(=O)NH(CH_2)_4$NH-, -$NH(CH_2)_4NHC(=O)CH_2$NH-, -$NH(CH_2)_2C(=O)NH(CH_2)_3$NH-, -$NH(CH_2)_3NHC(=O)(CH_2)_2$NH-, -$NH(CH_2)_3C(=O)NH(CH_2)_2$NH- and –$NH(CH_2)_2NHC(=O)(CH_2)_3$NH-; or

where Zaa_1 and Zaa_2 are selected from L-lysine and ornithine; and

L is selected from –C(=O)$(CH_2)_4$C(=O)-, -C(=O)$(CH_2)_5$C(=O)-, -C(=O)$(CH_2)_6$C(=O)-, -C(=O)$(CH_2)_7$C(=O)-, -C(=O)$(CH_2)_2O(CH_2)_2$C(=O)-, -C(=O)$(CH_2)N^+H_2(CH_2)_2$C(=O)-, -C(=O)$(CH_2)S(CH_2)_2$C(=O)-, -C(=O)$CH_2C(=O)NH(CH_2)_2$C(=O)-, -C(=O)$(CH_2)_2NHC(=O)CH_2$C(=O)-, -C(=O)$(CH_2)_2SS(CH_2)_2$C(=O)-, -C(=O)$(CH_2)_2O(CH_2)_3$C(=O)-, -C(=O)$(CH_2)_2N^+H_2(CH_2)_3$C(=O)-, -C(=O)$(CH_2)_2S(CH_2)_3$C(=O)-, -C(=O)$(CH_2)_2C(=O)NH(CH_2)_2$C(=O)-, -C(=O)$(CH_2)_2NHC(=O)(CH_2)_2$C(=O)-, -C(=O)$CH_2C(=O)NH(CH_2)_3$C(=O)-, -C(=O)$(CH_2)_3NHC(=O)CH_2$C(=O)-, -C(=O)$CH_2C(=O)NH(CH_2)_4$C(=O)-,

$-C(=O)(CH_2)_4NHC(=O)CH_2C(=O)-$, $-C(=O)(CH_2)_2C(=O)NH(CH_2)_3C(=O)-$, $-C(=O)(CH_2)_3NHC(=O)(CH_2)_2C(=O)-$, $-C(=O)(CH_2)_3C(=O)NH(CH_2)_2C(=O)-$ and $-C(=O)(CH_2)_2NHC(=O)(CH_2)_3C(=O)-$; or

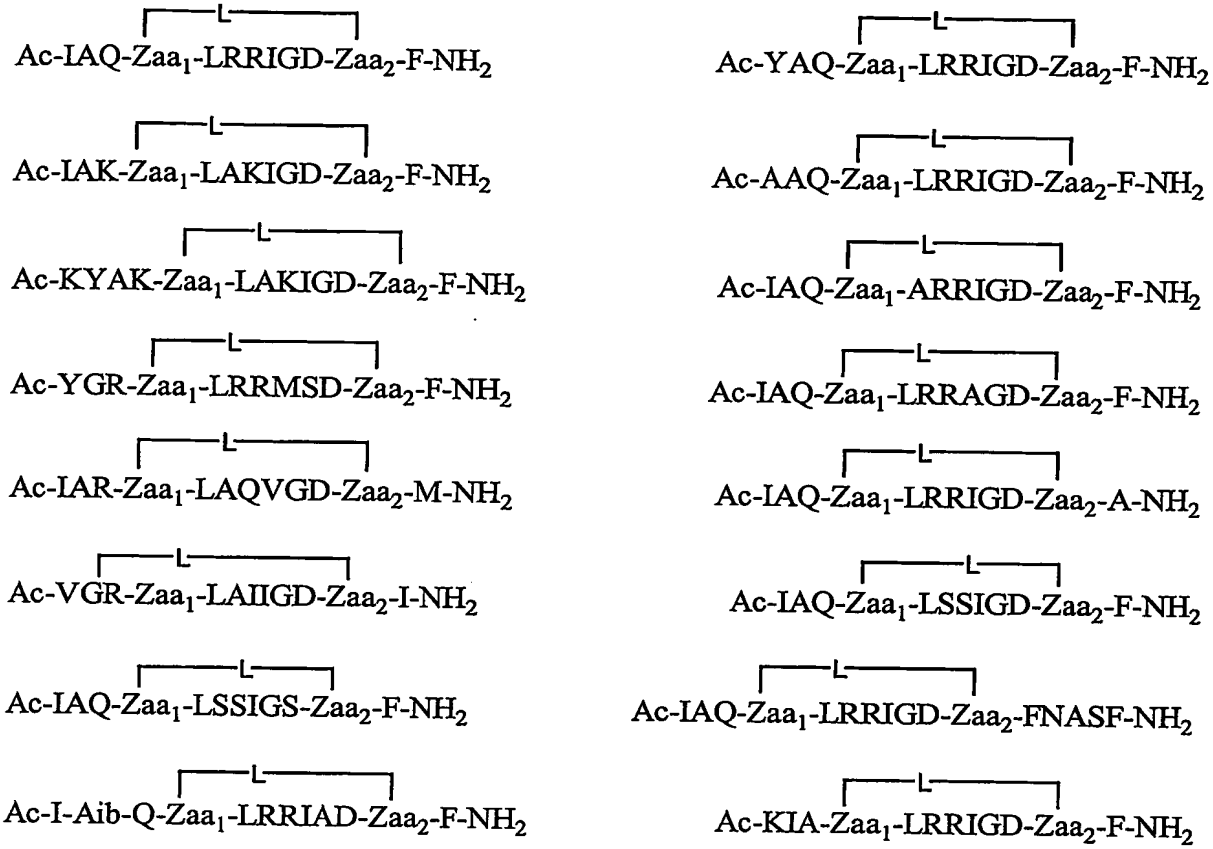
where Zaa_1 is selected from L-aspartic acid, L-glutamic acid and Zaa_2 is selected from L-lysine and ornithine; and

L is selected from $-NH(CH_2)_4C(=O)-$, $-NH(CH_2)_5C(=O)-$, $-NH(CH_2)_6C(=O)-$, $-NH(CH_2)_7C(=O)-$, $-NH(CH_2)_2O(CH_2)_2C(=O)-$, $-NH(CH_2)N^+H_2(CH_2)_2C(=O)-$, $-NH(CH_2)S(CH_2)_2C(=O)-$, $-NHCH_2C(=O)NH(CH_2)_2C(=O)-$, $-NH(CH_2)_2NHC(=O)CH_2C(=O)-$, $-NH(CH_2)_2SS(CH_2)_2C(=O)-$, $-NH(CH_2)_2O(CH_2)_3C(=O)-$, $-NH(CH_2)_2N^+H_2(CH_2)_3C(=O)-$, $-NH(CH_2)_2S(CH_2)_3C(=O)-$, $-NH(CH_2)_2C(=O)NH(CH_2)_2C(=O)-$, $-NH(CH_2)_2NHC(=O)(CH_2)_2C(=O)-$ $-NHCH_2C(=O)NH(CH_2)_3C(=O)-$, $-NH(CH_2)_3NHC(=O)CH_2C(=O)-$, $-NHCH_2C(=O)NH(CH_2)_4C(=O)-$, $-NH(CH_2)_4NHC(=O)CH_2C(=O)-$, $-NH(CH_2)_2C(=O)NH(CH_2)_3C(=O)-$, $-NH(CH_2)_3NHC(=O)(CH_2)_2C(=O)-$, $-NH(CH_2)_3C(=O)NH(CH_2)_2C(=O)-$ and $-NH(CH_2)_2NHC(=O)(CH_2)_3C(=O)-$; or

where Zaa_1 is selected from L-lysine and ornithine and Zaa_2 is selected from L-aspartic acid, L-glutamic acid; and

L is selected from $-C(=O)(CH_2)_4NH-$, $-C(=O)(CH_2)_5NH-$, $-C(=O)(CH_2)_6NH-$, $-C(=O)(CH_2)_7NH-$, $-C(=O)(CH_2)_2O(CH_2)_2NH-$, $-C(=O)(CH_2)N^+H_2(CH_2)_2NH-$, $-C(=O)(CH_2)S(CH_2)_2NH-$, $-C(=O)CH_2C(=O)NH(CH_2)_2NH-$, $-C(=O)(CH_2)_2NHC(=O)CH_2NH-$, $-C(=O)(CH_2)_2SS(CH_2)_2NH-$, $-C(=O)(CH_2)_2O(CH_2)_3NH-$, $-C(=O)(CH_2)_2N^+H_2(CH_2)_3NH-$, $-C(=O)(CH_2)_2S(CH_2)_3NH-$, $-C(=O)(CH_2)_2C(=O)NH(CH_2)_2NH-$, $-C(=O)(CH_2)_2NHC(=O)(CH_2)_2NH-$, $-C(=O)CH_2C(=O)NH(CH_2)_3NH-$, $-C(=O)(CH_2)_3NHC(=O)CH_2NH-$, $-C(=O)CH_2C(=O)NH(CH_2)_4NH-$, $-C(=O)(CH_2)_4NHC(=O)CH_2NH-$, $-C(=O)(CH_2)_2C(=O)NH(CH_2)_3NH-$, $-C(=O)(CH_2)_3NHC(=O)(CH_2)_2NH-$, $-C(=O)(CH_2)_3C(=O)NH(CH_2)_2NH-$ and $-C(=O)(CH_2)_2NHC(=O)(CH_2)_3NH-$.

36. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 1 selected from the group consisting of:



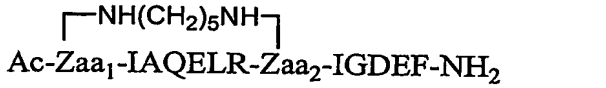
wherein Zaa_1 and Zaa_2 are as defined in claim 17 and L is a linker which tethers Zaa_1 and Zaa_2.

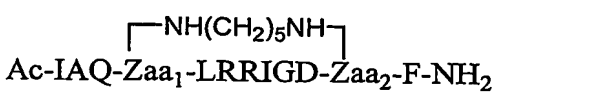
37. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 36 wherein Zaa_1 and Zaa_2 are independently selected from L-aspartic acid and L-glutamic acid and L is selected from the group consisting of $-NH(CH_2)_5NH-$, $-NH(CH_2)_6NH-$, $-NH(CH_2)_7NH-$, $-NHCH_2(=O)NH(CH_2)_2NH-$, $-NH(CH_2)_2NHC(=O)CH_2NH-$, $-NH(CH_2)_2O(CH_2)_3NH-$ and $-NH(CH_2)_2C(=O)NH(CH_2)_2NH-$.

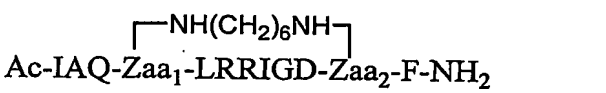
38. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 37 wherein L is selected from the group consisting of $-NH(CH_2)_5NH-$ and $-NHCH_2C(=O)NH(CH_2)_2NH-$.

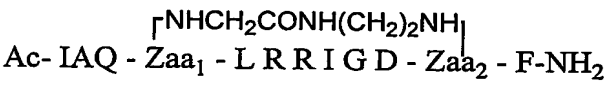
39. A conformationally constrained compound or pharmaceutically acceptable salt or

prodrug thereof according to claim 1 selected from the group consisting of:









wherein Zaa_1 and Zaa_2 are independently selected from L-aspartic acid and L-glutamic acid.

40. A conformationally constrained compound or pharmaceutically acceptable salt or prodrug thereof according to claim 39 wherein Zaa_1 and Zaa_2 are both L-glutamic acid.

41. A pharmaceutical composition comprising a conformationally constrained compound, or a pharmaceutically acceptable salt or prodrug thereof, the compound comprising an amino acid sequence (I):

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

wherein Haa_1, Haa_2, Haa_3 and Haa_4 are each independently an amino acid residue with a hydrophobic side chain or when n and m are both 1, one of Haa_1, Haa_2 and Haa_4 is optionally Xaa_1;

each Saa is an amino acid residue with a small side chain;

Naa is an amino acid residue with a negatively charged side chain;

Xaa_1, Xaa_2, Xaa_3, Xaa_4 and Xaa_5 are each independently an amino acid residue, Zaa_1 or Zaa_2;

R is H, an N-terminal capping group or an oligopeptide optionally capped by an N-terminal capping group;

R' is H, a C-terminal capping group or an oligopeptide optionally capped by a C-terminal capping group; and

m and n are 0 or 1, provided that at least one of m and n is 1;

wherein a conformational constraint is provided by a linker which tethers two amino acid residues, Zaa_1 and Zaa_2, in the sequence, together with one or more pharmaceutically acceptable carriers and optionally, other therapeutic and/or prophylactic ingredients.

42. An assay for identifying compounds which bind to a member of the Bcl-2 family of proteins, the assay comprising the steps of:

(a) providing a candidate compound to be tested;

(b) contacting a Bcl-2 family protein with the candidate compound and a peptide comprising the amino acid sequence:

IAQELRRIGDEFN

under conditions sufficient to allow the candidate compound and the peptide to bind to the Bcl-2 family protein; and

(c) determining whether the candidate compound has bound to the Bcl-2 family protein.

43. An assay according to claim 42 wherein the peptide has an amino acid sequence:

DLRPEIRIAQELRRIGDEFNETYTRR.

44. A method of regulating the death of a cell, comprising contacting the cell with an effective amount of a conformationally constrained compound, or a pharmaceutically acceptable salt or prodrug thereof, the compound comprising an amino acid sequence (I):

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

wherein Haa_1, Haa_2, Haa_3 and Haa_4 are each independently an amino acid residue with a hydrophobic side chain or when n and m are both 1, one of Haa_1, Haa_2 and Haa_4 is optionally Xaa_1;

each Saa is an amino acid residue with a small side chain;

Naa is an amino acid residue with a negatively charged side chain;

Xaa_1, Xaa_2, Xaa_3, Xaa_4 and Xaa_5 are each independently an amino acid residue, Zaa_1 or Zaa_2;

R is H, an N-terminal capping group or an oligopeptide optionally capped by an N-terminal capping group;

R' is H, a C-terminal capping group or an oligopeptide optionally capped by a C-terminal capping group; and

m and n are 0 or 1, provided that at least one of m and n is 1;

wherein a conformational constraint is provided by a linker which tethers two amino acid residues, Zaa_1 and Zaa_2, in the sequence.

45. A method of inducing apoptosis in unwanted or damaged cells comprising contacting said damaged or unwanted cells with an effective amount of a conformationally constrained compound, or a pharmaceutically acceptable salt or prodrug thereof, the compound comprising an amino acid sequence (I):

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

wherein Haa_1, Haa_2, Haa_3 and Haa_4 are each independently an amino acid residue with a hydrophobic side chain or when n and m are both 1, one of Haa_1, Haa_2 and Haa_4 is optionally Xaa_1;

each Saa is an amino acid residue with a small side chain;

Naa is an amino acid residue with a negatively charged side chain;

Xaa_1, Xaa_2, Xaa_3, Xaa_4 and Xaa_5 are each independently an amino acid residue, Zaa_1 or Zaa_2;

R is H, an N-terminal capping group or an oligopeptide optionally capped by an N-terminal capping group;

R' is H, a C-terminal capping group or an oligopeptide optionally capped by a C-terminal capping group; and

m and n are 0 or 1, provided that at least one of m and n is 1;

wherein a conformational constraint is provided by a linker which tethers two amino acid residues, Zaa_1 and Zaa_2, in the sequence.

46. A method of treatment and/or prophylaxis of a pro-survival Bcl-2 family member-mediated disease or condition, in a mammal, comprising administering to said mammal an effective amount of a conformationally constrained compound, or a pharmaceutically acceptable salt or prodrug thereof, the compound comprising an amino acid sequence (I):

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

wherein Haa_1, Haa_2, Haa_3 and Haa_4 are each independently an amino acid residue with a hydrophobic side chain or when n and m are both 1, one of Haa_1, Haa_2 and Haa_4 is optionally Xaa_1;

each Saa is an amino acid residue with a small side chain;

Naa is an amino acid residue with a negatively charged side chain;

Xaa_1, Xaa_2, Xaa_3, Xaa_4 and Xaa_5 are each independently an amino acid residue, Zaa_1 or Zaa_2;

R is H, an N-terminal capping group or an oligopeptide optionally capped by an N-terminal capping group;

R' is H, a C-terminal capping group or an oligopeptide optionally capped by a C-terminal capping group; and

m and n are 0 or 1, provided that at least one of m and n is 1;

wherein a conformational constraint is provided by a linker which tethers two amino acid residues, Zaa_1 and Zaa_2, in the sequence.

47. A method according to claim 46 wherein the disease or condition is an inflammatory condition, a cancer or an autoimmune disorder.

48. A method of treatment and/or prophylaxis of a disease or condition characterised by the inappropriate persistence or proliferation of unwanted or damaged cells in a mammal, comprising administering to said mammal an effective amount of a conformationally constrained compound, or a pharmaceutically acceptable salt or prodrug thereof, the compound comprising an amino acid sequence (I):

(I) $R\text{-}(Haa_1\text{-}Saa\text{-}Xaa_1\text{-}Xaa_2)_n\text{-}Haa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Haa_3\text{-}(Saa\text{-}Naa\text{-}Xaa_5\text{-}Haa_4)_m\text{-}R'$

wherein Haa_1, Haa_2, Haa_3 and Haa_4 are each independently an amino acid residue with a hydrophobic side chain or when n and m are both 1, one of Haa_1, Haa_2 and Haa_4 is optionally Xaa_1;

each Saa is an amino acid residue with a small side chain;

Naa is an amino acid residue with a negatively charged side chain;

Xaa_1, Xaa_2, Xaa_3, Xaa_4 and Xaa_5 are each independently an amino acid residue, Zaa_1 or Zaa_2;

R is H, an N-terminal capping group or an oligopeptide optionally capped by an N-terminal capping group;

R' is H, a C-terminal capping group or an oligopeptide optionally capped by a C-terminal capping group; and

m and n are 0 or 1, provided that at least one of m and n is 1;

wherein a conformational constraint is provided by a linker which tethers two amino acid residues, Zaa_1 and Zaa_2, in the sequence.